AMENDMENTS TO THE CLAIMS

1-26. (Cancelled)

27. (Currently amended) A method for purifying ~~AAV and/or~~ AAV particles, said method comprising providing AAV particles having ~~by using~~ a structural protein of adeno-associated virus (AAV)~~, wherein the structural protein~~ that comprises at least one mutation in VP3 located before and/or after at least one amino acid in the sequence selected from the group consisting of YKQIS SQSGA (SEQ ID NO: 2), YLTLN NGSQA (SEQ ID NO: 3), YYLSR TNTPS (SEQ ID NO: 4), EEKFF PQSGV (SEQ ID NO: 5), NPVAT EQYGS (SEQ ID NO: 6 and 7), LQRGN RQAAT (SEQ ID NO: 8), and NVDFT VDTNG(SEQ ID NO: 9), wherein said mutation ~~located on the virus surface which~~ brings about an alteration in the chromatographic properties of the virus; and purifying said AAV particles.

28. (Currently amended) The method as claimed in claim 27, wherein the alteration in the chromatographic properties makes possible an improvement in the purification relative to purification of wild-type AAV, the improvement being selected from the group consisting of a concentration of the virus to higher titers, a concentration of the virus particles to higher titers, a purification to greater purity, and a more efficient purification.

29. (Previously presented) The method as claimed in claim 27, wherein the mutation brings about a negligible reduction in the infectivity of the virus.

30-32. (Cancelled).

33. (Previously presented) The method as claimed in claim 27, wherein the structural

protein is derived from the group consisting of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, and other AAV serotypes derived therefrom.

34. (Previously presented) The method as claimed in claim 27, wherein the mutation in the structural protein is selected from the group consisting of a point mutation, a mutation of more than one amino acid, one or more deletion(s), one or more insertion(s), and a combination of said modifications.

35. (Cancelled).

36. (Currently amended) The method as claimed in claim ~~35~~ 27, wherein the mutation comprises an inserted amino acid sequence ~~is~~ selected from the group consisting of a ligand of a receptor, the receptor of a ligand, an antibody, part of an antibody, an antibody epitope, an antigen, an antigen epitope, a hormone, a hormone receptor, an enzyme, an enzyme substrate, a lectin, sugar-bearing amino acids, sugar-bearing amino acids from a histidine-rich peptide (His tag), a multiply charged peptide, glutathione S-transferase (GST tag), an F_c part of an antibody, an immunoglobulin-binding domain, protein A, ~~or~~ protein G, an immunoglobulin-binding domain of protein A, an immunoglobulin-binding domain part of protein G, a nucleic acid binding site, a heparin binding site, a specific ligand, a specific receptor, an integrin, a cytokine, a receptor binding domain of a cytokine, a growth factor, single-chain antibodies which bind to a cell surface receptor, an antibody against cell surface structures, an epitope, and an antibody-binding structure.

37. (Currently amended) The method as claimed in claim ~~35~~ 34, wherein a peptide which has the sequence QAGTFALRGDNPQG (SEQ ID NO: 1) is inserted into the structural protein.

38. (Previously presented) The method as claimed in claim 27, wherein the structural protein comprises at least one other mutation.

39. (Previously presented) The method as claimed in claim 38, wherein the other mutation(s) in the structural protein bring(s) about an alteration in the infectivity of the virus.

40. (Previously presented) The method as claimed in claim 38, wherein the other mutation(s) in the structural protein bring(s) about a reduction in the antigenicity of the virus.

41. (Previously presented) The method as claimed in claim 38, wherein the other mutation(s) in the structural protein is/are selected from the group consisting of one or more deletion(s), one or more insertion(s), and a combination of said modifications.

42. (Previously presented) The method as claimed in claim 38, wherein the insertion into the structural protein is selected from the group consisting of a cell membrane receptor ligand, a Rep protein, a Rep peptide, an immunosuppressive protein, an immunosuppressive peptide, a protein with a signal for double strand synthesis of the foreign gene, and a peptide with a signal for double strand synthesis of the foreign gene.

43. (Previously presented) The method as claimed in claim 38, wherein the insertion into the structural protein is selected from the group consisting of an integrin, a cytokine, a receptor binding domain of a cytokine, a growth factor, single-chain antibodies which bind to a cell surface receptor, an antibody against cell surface structures, an antibody-

binding structure, and an epitope.

44. (Cancelled)

45. (Previously presented) The method as claimed in claim 38, wherein the additional mutation(s) in the structural protein is/are located on the virus surface.

46. (Cancelled).

47. (Previously presented) The method as claimed in claim 38, wherein the additional mutation(s) is/are located at the N terminus of the structural protein.

48. (Cancelled).

49. (Previously presented) The method as claimed in claim 38, wherein the additional mutation(s) in the structural protein is/are brought about by one or more insertions in the XhoI cleavage site of the VP1-encoding nucleic acid.

50. (Cancelled).

51. (Previously presented) The method as claimed in claim 38, wherein the additional mutation(s) in the structural protein is/are brought about by one or more insertions in the BsrBI cleavage site of the VP1-encoding nucleic acid.

52. (Cancelled).

53. (Previously presented) The method as claimed in claim 38, wherein the additional

mutation(s) in the structural protein is/are brought about by one or more deletions between the BsrBI-HindII cleavage sites of the VP1-encoding nucleic acid, and one or more insertions.

54. (Cancelled).

55. (Previously presented) The method as claimed in claim 27, wherein the additional mutation(s) in the structural protein is/are brought about by one or more deletions between the XhoI-XhoI cleavage sites of the VP1-encoding nucleic acid.

56. (Cancelled).

57. (Previously presented) The method as claimed in claim 38, wherein the additional mutation(s) is/are brought about by one or more deletions between the BsrBI-HindII cleavage sites of the VP1-encoding nucleic acid.

58. (Cancelled).

59. (Previously presented) The method as claimed in claim 38, wherein one or more additional insertion(s) in VP3 is/are located before and/or after at least one amino acid in the sequence selected from the group consisting of YKQIS SQSGA (SEQ ID NO: 2), YLTLN NGSQA (SEQ ID NO: 3), YYLSR TNTPS (SEQ ID NO: 4), EEKFF PQSGV (SEQ ID NO: 5), NPVAT EQYGS (SEQ ID NO: 6 and 7), LQRGN RQAAT (SEQ ID NO: 8), and NVDFT VDTNG (SEQ ID NO: 9).

60-64. (Cancelled).

65. (New) The method as claimed in claim 36, wherein the inserted amino acid sequence is between 5 and 30 amino acids in length.